131.49 130.24

6.69 7.84

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Database: Issued_Patents_NA:*
Database sequences: 207703
Database length: 57918730
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Query: US-08-962-560A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 About: Results were produced by the GenCore software, Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OM of: US-08-962-560A-4 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query length: 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Command line parameters
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search time (sec): 62.100000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -MODEL-frame+_D2n.model -DEV-xlp
-MCDEL-frame+_D2n.model -DEV-xlp
-C-CeyCgnl.1/USPTO_spool/US08962560/runat_03022000_141755_3093/app_query.fasta.1
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-GAPEXT-4.000 -MINKATCH-0.100 -LOOPCL-0.000 -LOOPEXT-0.000
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-FGAPOP-6.000 -FGAPEXT-7.000 -YGAPOP-10.000 -YGAPEXT-0.500
-DELOP-6.000 -DELEXT-7.000 -START1 - MATRIX-blosum62
-TRANS-human40.cdi -LIST-45 -DCCALIGN-200 -THR_SCORE-PCT
-ALIGN-15 -MODE-LOCAL -OUTFMT-pfs -NORM-ext -MINLEN-0
-MAXLEN-100000 -USER-US08962560 -NCPU-6 -ICPU-3 -NO_XLDXY -WAIT
                                       Issued_Patents_NA:*
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                                                                 1848
1401
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                                                                                                                             alignment_block:
US-08-962-560A-4 x US-08-463-081B-9
                                                                                                                                                                                                                               alignment_scores:
                                                                                                                                                                            Quality:
Ratio:
Percent Similarity:
                                                                                                Align seg 1/1
                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                  10
                                                               14 SerProAlaAlaGluProArgArgArgSerGluProSerSerSerSerSe 30
30 rSerSerSerProAla...AlaProValArg...
                                                                                                                                                                                                                                                                                               NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
ZIP: 9007
                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
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                                GCCCCGGGAGCCTACCCAGCACGCGCTCCGCGCCCACTGGTTCCCTCCAG
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249.50 1.835 45.791

Percent

Length: Gaps: t Identity:

297 10 27.946

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seq_documentation_block:
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                                                                                                                                                                                                                                                                    MEDIDIM TYPE: FLOPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-POS/MS-DOS
SOFTWARE: Patentin Release #1.0,
SOFTWARE: Version #1.25
CURRENT APPLICATION NUMBER: US/08/463,081B
FILING DATE: 5-UN-1995
PRIOR APPLICATION NUMBER: US 08/104,736
FILING DATE: 10-AUG-1993
PRIOR APPLICATION NUMBER: US 07/796,066
FILING DATE: 20-NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: V1y1ana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P66 38150 (DART-050)
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECAN: (213) 622-7700
TELECAN: (213) 622-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9, Application US/08463081B Patent No. 5871960 Patent No. 5871960 5837487
                                                                                                                                                                                                   TELEFAX: (213) 489-421
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NERAL INFORMATION:
APPLICANT: Smith, Kendall A. & Beadling, Carol
APPLICANT: Smith, Nucleic Acids Encoding CR5 F
TITLE OF INVENTION: Nucleic Acids Encoding CR5 F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                      STRANDEDNESS: single
                                                                                                                                                      TYPE: nucleic acid
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: California
                                                                                                                                                                           1960 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: PRETTY, SCHROEDER & POPLAWSKI 444 South Flower St. - Suite 1900
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CDS
112..886
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GENERAL INFORMATION:

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160 ACTGGGCAGCGGCCCCTGTGGGCCCCGTCCCTGGAACTGCCCAAGCCAGT 209 47	40	μ ωυ	Align seg 1/1 to: US-08-461-379A-9 from: 1 to: 1960 14 SerProAlaAlaGluProArgArgArgSerGluProSerSerSerSerSe 30 ::: ::: ::: 10 Grococcasarocmacrosaconargaroccarocaconargamentoccara 59	alignment_block: US-08-962-560A-4 x US-08-461-379A-9	alignment_scores: Quality: 249.50 Ratio: 1.835 Percent Similarity: 45.791 Percent Identity: 27.946	TITLE OF INVENTION: Nucleic Acids Encoding CR5 Polypeptide, TITLE OF INVENTION: Vector and Transformed Cell Thereof, and TITLE OF INVENTION: Expression Thereof INTEL OF INVENTION: INTEL OF IN
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seq_documentation_block:
Sequence 9, Application US/08462390B;
Patent No. 5882894
GENERAL INFORMATION:
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       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                    APPLICANT: Smith, K. A., & Beadling, C.
TITLE OF INVENTION: Nucleic Acids Encoding CR8 Polypeptide, Vector and
TITLE OF INVENTION: Transformed Cell Thereof, and Expression Thereof
NUMBER OF SEQUENCES: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             845 GGCGCATGGCCGACTACCTCCGACAGTACCCCTTCCAGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             169 GlnArgArgValArgProLeuGlnGluLeuCysArg......GlnAr 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                610 TGCACTGCTGATACCCGAAGCGACAGCCCCGATCCTGCTCCCACCCCGGC 659
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   210 CATGCAGCCCTTGCCTGGGGGCCTTCCTCGAGGAGGTGGCAGAGGGTA 259
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                                                                                                                                                  ADDRESSEE:
                                                                           COUNTRY:
                                                                                                       STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tLeuGlyAlaPro.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGAAGAAGTGCCCGCAGCCTGCAACACCTGTGCCGCCTTGTCATCAACCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .....ThrPheAspCysLeuPheGluLeuGluHisTyrValAla... 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   roValGlyThrPheLeuValArgAspSerArgGlnArgAsnCysPhePhe 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TyrArgArgIleThrArgThrSerAlaLeuLeuAspAlaCysGlyPheTy 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..ProAlaProGlyAspThrHisPheArgThrPheArgSerHisSerAsp
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                                                                                                                           Valley Forge
                                                                                               Pennsylvania
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Floppy disk
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alignment_block:
US-08-962-560A-4 x US-08-462-390B-9
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Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (610)407-070: NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: DA TELECOMMUNICATION INFORMATION: TELEPHONE: (610)407-0700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: USSN 08/104/736
FILING DATE: 10-AUG-1993
APPLICATION NUMBER: USSN 07/796,066
FILING DATE: 20-NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: V1v1ana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REGISTRATION NUMBER: 30,930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                      160 ACTGGGCAGCGGCCCCTGTGGGCCCCGTCCCTGGAACTGCCCAAGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS LENGTH: 1960 base pai
                                                    260 CCCCAGCCCAGACAGAGAGTGAGCCAAAGGTGCTGGACCCAGAGGAGGAT 309
                                                                                                                                                                                              210 CATGCAGCCCTTGCCTGGGGGCCTTCCTCGAGGAGGTGGCAGAGGGTA 259
                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
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PRIOR APPLICATION DATA:
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49 ..ProAlaProGlyAspThrHisPheArgThrPheArgSerHisSerAsp
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                                                                                      65 TyrArgArgIleThrArgThrSerAlaLeuLeuAspAlaCysGlyPheTy 81
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TOPOLOGY: lir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: USSN 08/330,108 FILING DATE: 27-OCT-1994
                                                                                                                                                                                                                                  .....ProArgProCysProAlaVal..... 46
                                                                                                                                                                                                                                                                                                                                                                                                                  CCGCCGCCGTCCAGCCGAGTCCCCACTCCGGAGTCGCCGCTGCCGGGGG 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCCCCGGGAGCCTACCCAGCACGCGCTCCGCGCCCACTGGTTCCCTCCAG
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(610)407-0701
(610)407-0701
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Percent Identity:
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seq_name: /cgn1_6/ptodata/2/ina/5D_COMB.seq:US-08-918-206-2
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CURRENT APPLICATION NUMBER: US/08/918,206
FILING DATE: Fled Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/918,206
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08918206 Patent No. 5919661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                131 eGlnAlaGlyArgPheHisLeuAspGly.....SerArgGlu.... 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182 gIleValAlaAlaValGlyArgGluAsnLeuAlaArgIleProLeuAsnP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         610 TGCACTGCTGATACCCGAAGCGACAGCCCCGATCCTGCTCCCACCCCGGC 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                560 TCCTGGCCTTTCCGGATGTGGTCAGCCTTGTGCAGCACTATGTGGCCTCC 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               115 AlaLeuSerValLysMetAlaSerGlyProThrSerIleArgValHisPh 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         360 TTGGGGTTCCATTACGGCCAGCGAGGCCCGACAACACCTGCAGAAGATGC
                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         845 GGCGCATGGCCGACTACCTCCGACAGTACCCCTTCCAGCTC 885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     169 GlnArgArgValArgProLeuGlnGluLeuCysArg......GlnAr
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Hillman, Jennifer L.
APPLICANT: Guegler, Karl
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
RITLE OF INVENTION: CYTOKINE INDUCIBLE REGULATORY
FITTLE OF INVENTION: PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                    ORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 UMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                               ZIP: 94304
                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                           STREET:
                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                  Palo Alto
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                                                                                                                                                                                                                                                                                                                                                                           E: Incyte Pharmaceuticals, Inc. 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                         USA
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alignment_block:
US-08-962-560A-4 x US-08-918-206-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 ACCCCGTGCCCGCAGCTCGGGCGCGCCGCGCAGCCGATCAGTGGGTGACC 230
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LENGTH: 2587 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                        381 CCCCAGCTCGGGCGACCTGTCTTTGCCGCGGTGACCCTTCTCTCATG 430
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IMMEDIATE SOURCE:
LIBRARY: BRSTNOT13
CLONE: 2787140
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                                      101 rPheLeuValArgAspSerArgGlnArgAsnCysPhePheAlaLeuSerV 118
                                                                                    581 ATGACTGTTAATGAAGCCAAAGAGAAATTAAAAGAGGCACCAGAAGGAAC
                                                                                                                                                                          531 TCTGGCGAAGGCTGCGGGAGCTCGGTCAGACAGGATGGTACTGGGGAAGT 580
                                                                                                                                                                                                                                                              481 CCAGTGGGGGACCGCGGGGTCGGCGGAGGCGATCCCGCAGGCGGCGCG 530
                                                                                                                                                                                                                                                                                                                                                  431 ACCCTGCGGTGCCTTGAAGCCTCCGGGAATGGCGGGGAAGGGAACGCGGAG 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       231 GCGGCTGCGAGGCGACTTTGTCATCCGTCCTCCAGGATCTGGGGAGAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX:
                                                                                                                          LeuSerValHisGlyAlaHisGluArgLeuArgAlaGluProValGlyTh 101
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TTTCTTGATTAGAGATAGCTCGCATTCAGACTACCTACTAACAATATCTG
                                                                                                                                                                                                                                                                                                  .....SerHisSerAspTyrArgArgI 68
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1.743
46.154
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Gaps: 10
Percent Identity: 27.425
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seq_documentation_block:
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Patent No. 5871960 5837487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 33, Application US/08463081B
                                                                                    TELEFAX: (213) 489-4210
INFORMATION FOR SEQ ID NO: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION: APPLICANT: Smith,
                      SEQUENCE CHARACTERISTICS:
LENGTH: 774 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/104,736
FILING DATE: 10-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/796,066
FILING DATE: 20-NOV-91
ATTORNEY/AGENT INFORMATION:
                                                                                                                              NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P66 38150 (DART-060)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Smith, Kendall A. & Beadling, Carol TITLE OF INVENTION: Nucleic Acids Encoding CR5 Polypeptide, TITLE OF INVENTION: Vector and Transformed Cell Thereof, and Expression Thereof NUMBER OF SEQUENCES: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  881 ACCAAACCGCTC...TACACGTCAGCACCATCTCTGCAGCATCTCTGTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118 allysMetAlaSerGlyProThrSerIleArgValHisPheGlnAlaGly
                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI STREET: 444 South Flower St. - Suite 1900 CITY: Los Angeles STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/
FILING DATE: 5-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGCGGACAGGTCCAGAAGCCCCCCGGAACGGCACTGTTCACCTTTATCTG
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; MOLECULE TYPE:
US-08-463-081B-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-08-962-560A-4 x US-08-463-081B-33
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                                                                                                           181
                                                                                                                                                                                                   167
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                                                                                                                                                                                                                                                                                                                                                                                                                      487 TATGTGGCCTCCTGCACTGCTGATACCCGAAGCGACAGCCCCGATCCTGC
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195 leProLeuAsnProValLeuArgAspTyrLeuSerSerPheProPheGln 211
                                                                                                                                                                                                                                              587 CACTGCCTGCTCCACCAGCCACTGCTGTACACCTAAAACTGGTGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17 AlaGluProArgArgArgSerGluProSerSerSerSerSerSerSerSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCAGGCCACGCATCCTGGCCTTTCCGGATGTGGTCAGCCTTGTGCAGCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           eArgValHisPheGlnAlaGlyArgPheHisLeuAspGly....... 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       euArgAlaGluProValGlyThrPheLeuValArgAspSerArgGlnArg 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCAGAGGAGGATCTGCTGTGCATAGCCAAGACCTTCTCCTACCTTCGGGA 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGGCAGAGGGTACCCCAGCCCAGACAGAGAGTGAGCCAAAGGTGCTGGAC 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCCCAAGCCAGTCATGCAGCCCTTGCCTGCGGGGCCTTCCTCGAGGAGG
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                                                                  TGTCATCAACCGTCTGGTGGCCGACGTGGAC......TGCC
                                                                                                                                                       CCCTTTGTACGCAGAAGAAGTGCCCGCAGCCTGCAACACCTGTGCCGCCT 686
                                                                                                                                                                              .....LeuArgGlnArgArgValArgProLeuGlnGluLeuCysArg. 180
                                                                                                                                                                                                                                                                                                                                   TCCCACCCCGGCCCTGCCTATGCCTAAGGAGGATGCGCCTAGTGACCCAG 586
                                                                                                                                                                                                                                                                                                                                                                          aProArgArgMetLeuGlyAlaPro....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 aCysGlyPheTyrTrpGlyProLeuSerValHisGlyAlaHisGluArgL 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SerHisSerAspTyrArgArgIleThrArgThrSerAlaLeuLeuAspAl 77
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SOFTWARE:

COUNTRY:

90071

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seq_documentation_block:
                                                                                                                                                                                                                                                             alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: US-08-461-379A-33
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                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
                                                                                                                                                                                                 Align seg 1/1 to: US-08-461-379A-33
                                                                                                                                                                                                                                        US-08-962-560A-4 x US-08-461-379A-33
                                                                                                                                                                                                                                                                                                  Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 33, Application US/08461379A Patent No. 5871961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (610)470-0
TELEFAX: (610)470-070
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION: APPLICANT: Smith,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE, DOCKET NUMBER: DA
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 5-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/330,108; 08/104,736
APPLICATION NUMBER: 6 07/796,066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 27-CCT-1994; 10-AUG-1993 & 20-NOV-91 ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      722
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ADDRESSEE: Ratner &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                           87
                                                                              33 rProAlaAlaProValArgProArgProCysProAlaVal.....
                                                                                                                       37
                                                                                                                                                          17 AlaGluProArgArgArgSerGluProSerSerSerSerSerSerSerSe 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
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                                                                                                                     GCTGTGGAGCGGACTGGGCAGCGGCCCTGTGGGCCCCGTCCCTGGAACT 86
                                           GCCCAAGCCAGTCATGCAGCCCTTGCCTGCTGGGGGCCTTCCTCGAGGAGG 136
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.....ProAlaProAlaProGlyAspThrHisPheArgThrPheArg 60
                                                                                                                                                                                                                                                                                                                                           Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Smith, Kendall A. & Beadling, Carol
VENTION: Nucleic Acids Encoding CR5 Polypeptide,
VENTION: Vector and Transformed Cell Thereof, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DART-070
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seq_documentation_block:
; Sequence 33, Application US/08462390B
; Patent No. 5882894
                                                                                                                                                                                                                                                                                                                                                    seq_name: /cgnl_6/ptodata/2/ina/5C_COMB.seq:US-08-462-390B-33
                                                                                                                         GENERAL INFORMATION:
APPLICANT: Smith, K. A., & Beadling, C.
TITLE OF INVENTION: Nucleic Acids Encoding CR8 Polypeptide, Vector and
TITLE OF INVENTION: Transformed Cell Thereof, and Expression Thereof
NUMBER OF SEQUENCES: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         155
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                                       CITY: Valley Forge
STATE: Pennsylvania
                COUNTRY:
                                                                                 ADDRESSEE:
                                                                                                           ADDRESSEE:
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19482
                                     Pennsylvania
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                                                                                                        Ratner & Prestia
                                                                                 (B) STREET:One Westlakes-Berwyn
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COMPUTER READABLE FORM

MEDIUM TYPE: COMPUTER: II

Floppy disk

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TELEPHONE: (610)407-0700
TELEPHONE: (610)407-0701
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 774 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TYPE: TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-462-390B-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
US-08-962-560A-4 x US-08-462-390B-33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: USSN 08/104,736
FILING DATE: 10-AUG-1993
APPLICATION NUMBER: USSN 07/796,066
FILING DATE: 20-NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: V1V1Ana Amzel, ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: DART-040
                                                                                       337
                                                                                                                                                                                                                                                                     387 ACGCATTGAGTATGCCGACTCCAGCTTCCGTCTGGACTCCAACTGCTTGT 436
                                                                                                                                                                             187 CCAGAGGAGCATCTGCTGTGCATAGCCAAGACCTTCTCCTACCTTCGGGA 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/462,390B FILING DATE: 5-JUNE-1995 PRIOR APPLICATION DATA:
                                                                                                                                                                                                         94 euArgAlaGluProValGlyThrPheLeuValArgAspSerArgGlnArg 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: DATELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                     61 SerHisSerAspTyrArgArgIleThrArgThrSerAlaLeuLeuAspAl 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33 rProAlaAlaProValArgProArgProCysProAlaVal..... 46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37 GCTGTGGAGCGGACTGGGCAGCGGCCCCTGTGGGCCCCGTCCCTGGAACT 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: USSN 08/330,108
FILING DATE: 27-OCT 1994
APPLICATION NUMBER: USSN 08/104,736
                                                                                   aCysGlyPheTyrTrpGlyProLeuSerValHisGlyAlaHisGluArgL 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGGCAGAGGGTACCCCAGCCCAGACAGAGTGAGCCAAAGGTGCTGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCCCAAGCCAGTCATGCAGCCCTTGCCTGCTGGGGGCCTTCCTCGAGGAGG 136
                       eArgValHisPheGlnAlaGlyArgPheHisLeuAspGly....... 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .......ProAlaProAlaProGlyAspThrHisPheArgThrPheArg 60
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Ratio:
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1.837
51.394
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Percent Identity: 29.084
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                                                                                                                                                                                                                                                                     286
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COMPUTER: IEM PC COMPATIBLE COPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: ASCII text CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/259,264 FILING DATE: 10-JUN-1994 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: Myers, Louis REGISTRATION NUMBER: JDP-021 FILECOMMUNICATION INFORMATION: TELEPHONE: (617) 227-5941 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 5737 base pairs TYPE: nucleic acid STRANDEDNESS: slingle TOPOLOGY: linear MOLECULE TYPE: CDNA FRANUTURE: CDNA	seq_documentation_block: Sequence 1, Application US/08259264 Patent No. 5650293 GENERAL INFORMATION: APPLICANT: White, Morris F. TITLE OF INVENTION: pp60PIK: A DOWNSTREAM ELEMENT IN INSULIN SIGNALING NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS: ADDRESSEE: LAHYUE & COCKFIELD STREET: 60 STATE STREET, SUITE 510 CITY: BOSTON STATE: MASSACHUSETTS COUNTRY: USA 2IP: 02109 COMPUTER READABLE FORM:	195 leProLeuAsnProValLeuArgAspTyrLeuSerSerPheProPheGln 211 :: 722 TGCCACTGCCCCGGCGCATGGCCGACTACCTCCGACAGTACCCCCTTCCAG 771 212 Ile 212 ::: 772 CTC 774 seq_name: /cgnl_6/ptodata/2/ina/5A_COMB.seq:US-08-259-264-1	166	141 erArgGluThrPheAspCysLeuPheGluLeuLeuGluH1s 154

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seq_documentation_block:
; Sequence 1, Application US/08076011
; Patent No. 5521069
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US-08-259-264-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: /cgn1_6/ptodata/2/ina/5A_COMB.seq:US-08-076-011-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-08-962-560A-4 x US-08-259-264-1
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Quality:
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                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1615 AGATGGTACCTTCTTAGTTCGTGATGCCTCAACGAAAATGCAGGGGGATT 1664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1856 CAACAGGATCAGTTGGTAAAAGAAGATAACATTGATGCAGTAGGTAAA 1903
                                                                                                                                                     APPLICANT: KIMURA, Chiharu
APPLICANT: OHKUBO, Shoichi
TITLE OF INVENTION: NOVEL DNA AND USE THEREOF
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    131 PheGlnAlaGlyArgPheHisLeuAspGlySerArgGlu.....ThrPh 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        114 heAlaLeuSerValLysMetAlaSerGlyProThrSerIleArgValHis 130
                                                                                                                                                                                                                                                                                          APPLICANT: ONDA, Haruo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50 aProGly.....AspThrHisPheArgThrPheArgSerHisSerAspT 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34 ProAlaAlaProValArgProArgProCysProAlaValProAlaProAl 50
COUNTRY: US
                                                                          STREET:
                                                                                                      ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCAGCTCTTCCACCAAAGCCA...CCTAAGCCAATGACTCCAGCAGTCAC 1515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGTACAATCCCAAACTCGACGTGAAGCTGACGTACCCAGTATCCAGATTC 1855
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATCGGGATGGTAAATAT.......GGCTTCTCTGAGCCCCTGACGTT 1755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           oValGlyThrPheLeuValArgAsp...SerArgGlnArgAsnCysPheP 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGGGGAGATATTTCCAGGGAAGAGGTAAATGACAAATTGCGGGACATGCC 1614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TrpGlyProLeuSerValHisGlyAlaHisGluArgLeuArgAlaGluPr 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATACATTGACTTTGAGGAAGGGAGGAAATAATAAATTAATAAAGATCTAT 1714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .....GlnGluLeuCysArgGlnArgIleValAlaAlaValGlyArg 189
                                                    Boston
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                                                                       130 Water Street
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                                                                                                      DAVID G. CONLIN; DIKE, BRONSTEIN ROBERTS & CUSHMAN
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1.392
53.012
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Percent Identity: 27.108
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LOCATION:

LOCATION:

LOCATION:

COCATION:

US-08-076-011-1
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US-08-962-560A-4 x US-08-076-011-1
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Percent Similarity:
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REFERENCE/DOCKET NUMBER: 4115
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
TELEFAX: (617)523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 17041 base pairs
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APPLICATION NUMBER: US/08/076,011
FILING DATE: 11-JUN-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/047,246
FILING DATE: 13-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                    6696 GTAGCAGCAGCAGAAGCCGCAGCTTCAGAGGCAGCCGGAGAGACCTCGGA 6745
                                                                                                                                                                                                                                                            6781 GCCCGCGCTCCTACAAAGGCGGGCTAGCCGCCCGCCCTCTCCCCTTGCCT
                                                                                                                                                                                                                                                                                                                                                NAME:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
05.07/741,676
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: RESNICK, DAVID S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                   35 laAlaProValArgProArgProCysProAlaValProAlaProAlaPro 51
                                                                                                                                                                                                                                                                                                                                                                                  18 uProArgArgArgSerGluProSerSerSerSerSerSerSerFroA 35
                                                                                                                                                                                                               52 GlyAspThrHisPheArgThrPheArgSerHisSerAspTyrArgArgIl 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 ValAlaArgAsnGlnValAlaAlaAspAsnAlaIleSerProAlaAlaGl 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
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FILING DATE: 07-AUG-1991
                                        euSerValHisGlyAlaHisGluArgLeuArgAlaGluProValGly... 100
                                                                                                                            eThrArgThrSerAlaLeuLeuAspAlaCysGlyPheTyrTrpGlyProL 85
                                                                                                                                                                       TCCTCCCCTTCTTTCTGACTTTC..... 6854
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11602..11787)
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1.235
43.946
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Percent Identity:
.CGCCTGCTTCTTCCTCCGGGTGGACTT 6896
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10
27.803
                                                                                     6858
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; LENGTH: 2508
; TYPE: DNA
; ORGANISM: human
US-08-850-993-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: /cgn1_6/ptodata/2/ina/5D_COMB.seq:US-08-850-993-1
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                                                                                                                                                                                                US-08-962-560A-4 x US-08-850-993-1
                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Hansen, Torben
APPLICANT: Hansen, Carsten
APPLICANT: Adersen, Oluf B.
TITLE OF INVENTION: Mutant cDNA Encoding The p85alpha
TITLE OF INVENTION: Subunit Of Phosphatidylinositol 3-Kinase
FILE REFERENCE: 4802.200-US
CURRENT FILING DATE: 1997-05-05
EARLIER APPLICATION NUMBER: 0539/96
EARLIER FILING DATE: 1996-05-06
WINDERS OF SEC IN NOC. 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08850993 Patent No. 5955277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7170 CCGTCCTACCTGGCAGCTCTCCTGGCAGCGGGAGGAGTTGAAGGGTAAGG 7219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7029 ACGAGCCTCGGCAAACGA......GTCCCGCAGCTCCTCCTGCTGCT 7069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115
                                              943 CAGCCTGCACCAGCACTGCCTCCTAAACCACCAAAACCTACT..... 984
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               132 lnAlaGlyArgPheHisLeuAspGlySerArgGluThrPheAspCysLeu 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101
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57 gThrPheArgSerHisSerAspTyrArgArgIleThrArgThrSerAlaL 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     yArgGluAsnLeuAlaArg 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCTCTCGGGTGGTGACTCCAGCGCAGGAACTTGAAGAAGCGCTTTGCCCG :7169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rgGlnArgArgValArgProLeuGlnGlu.....LeuCysArg 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTCCTGGTTCTGCGCGTCTA......CAAACTTTTGAGCAGAAC 7028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   aLeuSerValLysMetAlaSerGlyProThrSerIleArgValHisPheG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACGGCCACCTTGCTCCGCGCGCTTCACCTCATCGCCCCCTCTTT.... 6941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .....ThrPheLeuValArgAspSerArgGlnArgAsnCysPhePheAl 115
                                                                                                                                                                                                                                                                                                                      Quality:
                                                                                                                                                                                                                                                                                                 Ratio:
                                                                                                                                                                                                                                                                       119.50
1.258
53.073
                                                                                                                                                                                                                                                                     Length: 179
Gaps: 7
Percent Identity: 24.581
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seq_name:
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                                               SOFTWARE: PATENTIN Release #1.0, Ver CURENT APPLICATION DATA:
APPLICATION NUMBER: US/07/906,349A FILING DATE: 30-JUN-1992 CLASSIFICATION: 435
PRIOR APPLICATION DATA: APPLICATION UMBER: 07/643,237
FILING DATE: 18-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1384 ..... TTACATGAATATAACACTCAGTTT 1407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1201 GGGAAATATGGCTTCTCTGACCCATTAACCTTCAGTTCTGTGGTTGAATT 1250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1119 GTCTACTAAAATGCATGGTGATTATACTCTTACACTAAGGAAAGGGGGAA 1168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1069 AATGAAAAACTTCGAGATACAGCAGACGGGACCTTTTTGGTACGAGATGC 1118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1019 CCTTACAAATGCTGAATGGTACTGGGGAGATATCTCGAGGGAAGAAGTG 1068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1169 ATAACAAATTAATCAAAATA......TTTCATCGAGAT 1200
                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Schlessinger, Joseph
APPLICANT: Skolnik, Edward Y.
APPLICANT: Margolis, Benjamin L.
TITLE OF INVENTION: A NOVEL EXPRESSION-CLONING METHOD FOR
TITLE OF INVENTION: IDENTIFYING TARGET PROTEINS FOR EUKARYOTIC TYROSINE KINASES
TITLE OF INVENTION: TARGET PROTEINS
TELECOMMUNICATION INFORMATION: TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          196 oLeuAsnProValLeuArgAspTyrLeuSerSerPhe 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          168 rgGlnArgArgValArgProLeuGlnGluLeuCysArgGlnArgIleVal 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151 uLeuGluHisTyrValAlaAlaProArgArgMetLeuGlyAlaProLeuA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123 lyProThrSerIleArgValHisPheGlnAlaGlyArgPheHisLeuAsp 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91 HisGluArgLeuArgAlaGluProValGlyThrPheLeuValArgAsp., 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74 euLeuAspAlaCysGlyPheTyrTrpGlyProLeuSerValHisGlyAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 419 Sever
                                                                                                                                                                                                                                                                                                                                                                                                    STATE: D.C
COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AATAAACCACTACCGGAATGAATCTCTAGCTCAGTATAATCCCAAATTGG 1300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .....AlaAlaValGlyArgGluAsnLeuAlaArgIlePr 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cgn1_6/ptodata/2/ina/5A_COMB.seq:US-07-906-349A-1
                                                                                                                                                                                                                                                                                                                                                                                20004
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419 Seventh Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                         USA
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alignment_block:
US-08-962-560A-4 x US-07-906-349A-1
                                                                                                                                                        seq_documentation_block:
                                                                                                                                                                                                   seq_name: /cgn1_6/ptodata/2/ina/5A_COMB.seq:US-08-167-035-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                        Patent No.
                                                                                                                              Sequence 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: ... SEQUENCE CHARACTERISTICS: LENGTH: 3372 base pairs TYPE: nucleic acid STRANDEDNESS: single STRANDEDNESS: single
                                                  GENERAL INFORMATION:
APPLICANT: Schles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            140 GlySerArgGlu......ThrPheAspCysLeuPheGluLe 151
                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  946 CAGCCTGCACCAGCACTGCCTCCTAAACCACCAAAACCTACT...... 987
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  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91 HisGluArgLeuArgAlaGluProValGlyThrPheLeuValArgAsp.. 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74 euLeuAspAlaCysGlyPheTyrTrpGlyProLeuSerValHisGlyAla 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rgGlnArgArgValArgProLeuGlnGluLeuCysArgGlnArgIleVal 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AATGAAAAACTTCGAGATACAGCAGACGGGACCTTTTTGGTACGAGATGC 1121
                                                                                                                                                                                                                                                                                                            oLeuAsnProValLeuArgAspTyrLeuSerSerPhe
                                                                                                                                                                                                                                                                                                                                                               AAAGAAGATAATATTGAAGCTGTAGGGAAAAAA......
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .ACTGTAGCCAACAACGGT......ATGAATAACAATATGT 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gThrPheArgSerHisSerAspTyrArgArgIleThrArgThrSerAlaL 74
                                                                                                                                                                                                                                                            .....TTACATGAATATAACACTCAGTTT 1410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AATAAACCACTACCGGAATGAATCTCTAGCTCAGTATAATCCCAAATTGG 1303
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                                                                                                                                                                                                                                                                                                                                                                                          .....AlaAlaValGlyArgGluAsnLeuAlaArgIlePr 196
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                                                                                                                                Application US/08167035
Schlessinger, Joseph
Skolnick, Edward Y.
Margolis, Benjamin L.
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1.258
53.073
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alignment_block:
US-08-962-560A-4 x US-08-167-035-1
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: US-08-167-035-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (212) 869-974
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: COTUZZI, LAUTA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7683
RELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: NOV.
TITLE OF INVENTION: IDE.
TITLE OF INVENTION: KIN.
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                      1072 AATGAAAAACTTCGAGATACAGCAGACGGGACCTTTTTGGTACGAGATGC 1121
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LENGTH: 3372 base pai
123 lyProThrSerIleArgValH1sPheGlnAlaGlyArgPheH1sLeuAsp 139 :: ||||::::::
                                                                                                                                                                                                                                                                                                                           988 .ACTGTAGCCAACAACGGT......ATGAATAACAATATGT 1021
                                                                                                                                                                                                                                                                                                                                                                                                               946 CAGCCTGCACCAGCACTGCCTCCTAAACCACCAAAACCTACT.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                            74 euLeuAspAlaCysGlyPheTyrTrpGlyProLeuSerValHisGlyAla
                                                                                                                                                                                                                                                                                                                                                                  57 gThrPheArgSerHisSerAspTyrArgArgIleThrArgThrSerAlaL 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                        41 ArgProCysProAlaValProAlaProAlaProGlyAspThrHisPheAr 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
TOPOLOGY: unl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/0
FILING DATE: 16-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: 10036-
ZIP: 10036-2711
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                                                                                                                                                                             HisGluArgLeuArgAlaGluProValGlyThrPheLeuValArgAsp.. 106
                                                                 GTCTACTAAAATGCATGGTGATTATACTCTTACACTAAGGAAAGGGGGAA 1171
                                                                                                          .SerArgGlnArgAsnCysPhePheAlaLeuSerValLysMetAlaSerG 123
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)EDNESS: double
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7: 10036-2711
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1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3372 base pairs
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43..2214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps: 7
Percent Identity: 24.581
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seq_name: /cgn1_6/ptodata/2/1na/5A_COMB.seq:US-08-167-035-48
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                                                                                   ; MOLECULE TYPE: US-08-167-035-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1254 AATAAACCACTACCGGAATGAATCTCTAGCTCAGTATAATCCCAAATTGG 1303
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                                        alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151 uLeuGluHisTyrValAlaAlaProArgArgMetLeuGlyAlaProLeuA 168
Ratio:
percent similarity:
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                                                                                                                                                                                     TELEX: 66141 PENNIE
                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                             REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 768
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATGTGAAATTACTTTATCCAGTATCCAAATACCAACAGGATCAAGTTGTC 1353
                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rgGlnArgArgValArgProLeuGlnGluLeuCysArgGlnArgIleVal 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTACATGAATATAACACTCAGTTT 1410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DDRESSEE:
                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
FILING DATE: 16-DE
                                                                                                                  TOPOLOGY:
                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                            ELEPHONE:
                                                                                                                                                            ENGTH:
                                                                                                                                                                                                                  ELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                10036-2711
                                Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New York
                                                                                                                                      nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ......AlaAlaValGlyArgGluAsnLeuAlaArgIlePr 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Margolis, Benjamin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schlessinger, Joseph
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                                                                                                                                                               3372 base pairs
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       119.50
1.258
53.073
                                                                                                                                                                                                                                                                                          Laura A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOVEL EXPRESSION CLONING METHOD FOR IDENTIFYING TARGET PROTEINS FOR EUKARYOTIC TYROSINE KINASES AND NOVEL TARGET PROTEINS
                                                                                                                                                                                                                      869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EDMONDS
                                                                                                                                                                                                                                                                                                                                                  US/08/167,035
                                                                                                                                                                                              48:
          Gaps: 7
Percent Identity: 24.581
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alignment_block:
US-08-962-560A-4 x US-08-167-035-48/rev
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                                                                                                                                                                                                                                                                                                                                                                 seq_name: /cgn1_6/ptodata/2/ina/5A_COMB.seq:US-08-208-887A-1
                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2427 CAGCCTGCACCAGCACTGCCTCCTAAACCCAAAACCTACT...... 2386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2351 CCTTACAAAATGCTGAATGGTACTGGGGAGATATCTCGAGGGAAGAAGTG
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APPLICANT:
APPLICANT:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                  CORRESPONDENCE ADDRESS:
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                                                                     COUNTRY:
                                                                                                                                                                                 FICANT: Skolnick, Edward Y.

PLICANT: Margolis, Benjamin L.

PLICANT: MARGOLIS, Benjamin L.

PLICANT: MARGOLIS, BENJAMIN CLONING METHOD FOR EUKARYOTIC TYROSINE ILE OF INVENTION: IDENTIFYING TARGET PROTEINS

PLE OF INVENTION: KINASES AND NOVEL TARGET PROTEINS
                                                                                                                                       DDRESSEE:
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                                                        10036-27
                                                                                      New York
                                                                                                                     E: PENNIE & EDMONDS
                                                                       10036-2711
                                                                                                                              the Americas
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alignment_block:
US-08-962-560A-4 x US-08-208-887A-1
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                                                                                                                                  1204 GGGAAATATGGCTTCTCTGACCCATTAACCTTCAGTTCTGTGGTTGAATT 1253
                                                                                                                                                                                                                   1172 ATAACAAATTAATCAAAATA...
                                                                 L254 AATAAACCACTACCGGAATGAATCTCTAGCTCAGTATAATCCCAAATTGG 1303
                                                                                               151 uLeuGluHisTyrValAlaAlaProArgArgMetLeuGlyAlaProLeuA 168
                                                                                                                                                                                                                                                                       1122 GTCTACTAAAATGCATGGTGATTATACTCTTACACTAAGGAAAGGGGGAA 1171
                                                                                                                                                                                                                                                                                                                                            1072 AATGAAAAACTTCGAGATACAGCAGACGGGACCTTTTTGGTACGAGATGC 1121
                                                                                                                                                                  140 GlySerArgGlu.....ThrPheAspCysLeuPheGluLe 151
                                                                                                                                                                                                                                     123 lyProThrSerIleArgValHisFheGlnAlaGlyArgPheHisLeuAsp 139
                                                                                                                                                                                                                                                                                                                                                                                                              1022 CCTTACAAAATGCTGAATGGTACTGGGGAGATATCTCGAGGGAAGAAGTG 1071
                                                                                                                                                                                                                                                                                                       107 .SerArgGlnArgAsnCysPhePheAlaLeuSerValLysMetAlaSerG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               988 .ACTGTAGCCAACAACGGT.....ATGAATAACAATATGT 1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                946 CAGCCTGCACCACCACTGCCTCCTAAACCACCAAAACCTACT..... 987
                                                                                                                                                                                                                                                                                                                                                                 91 HisGluArgLeuArgAlaGluProValGlyThrPheLeuValArgAsp.. 106
                                                                                                                                                                                                                                                                                                                                                                                                                                             74 euLeuAspAlaCysGlyPheTyrTrpGlyProLeuSerValHisGlyAla 90
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                               rgGlnArgArgValArgProLeuGlnGluLeuCysArgGlnArgIleVal 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 3372 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DO SOFTWARE: Patentin Rel. CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gThrPheArgSerHisSerAspTyrArgArgIleThrArgThrSerAlaL 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
(GTGAAATTACTTTATCCAGTATCCAAATACCAACAGGATCAAGTTGTC 1353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Coruzzi, Laura A. REGISTRATION NUMBER: 30,742 REFERENCE/DOCKET NUMBER: 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/0
FILING DATE: 11-MAR-1994
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EDNESS: double
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n_Release #1.0, Version #1.30
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alignment_block:
US-08-962-560A-4 x US-08-539-005-1
                                    Align seg 1/1 to: US-08-539-005-1 from: 1 to: 3372
                                                                                                                                                                                                                           ; NAME/KEY: LOCATION: US-08-539-005-1
                                                                                                                                                                          alignment_scores:
                                                                                                                           Ratio: Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: /cgn1_6/ptodata/2/ina/5C_COMB.seq:US-08-539-005-1
                                                                                                                                                                                                                                                                                                                                                                TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/167
FILING DATE: 16-DEC-1993
CLASSIFICATION: 435
ATTORNEY_AGENT INFORMATION:
NAME: COTUZZ1, Laura A.
REGISTRATION NUMBER: 30,742
41 ArgProCysProAlaValProAlaProAlaProGlyAspThrHisPheAr 57
                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 76
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      URRENT AFFILIATION MOBER: US/08/337,000
FILING DATE: 4-OCT-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
US 08/167,035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      _documentation_block;
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STATE: New York
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IVENTION: NOVEL EXPRESSION CLONING METHOD FOR IVENTION: LIDENTIFYING TARGET PROTEINS FOR EUKARYOTIC TYROSINE IVENTION: KINASES AND NOVEL TARGET PROTEINS
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                                                                                                               Percent Identity: 24.581
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96 87	8 4	68 04	51 54	04	23 72	07 22	91 72	74 22	57 88	46
OLeuAsnProValLeuArgAspTyrLeuSerSerPhe 208 ::::::	AlaAlaValGlyArgGluAsnLeuAlaArgIleDr 196 ::::: AAAGAAGATAATATTGAAGCTGTAGGGAAAAAA	rgGlnArgArgValArgProLeuGlnGluLeuCysArgGlnArgIleVal 184 ::: :::::::::::::::::::::::::::::::	ULeuGluHisTyrValAlaAlaProArgArgMetLeuGlyAlaProLeuA 168 	GlySerArgGluThrPheAspCysLeuPheGluLe 15 ::: :::	lyProThrSerIleArgValHisPheGlnAlaGlyArgPheHisLeuAsp 13 ::	SerArgGlnargAsnCysPhePheAlaLeuSerValLysMetAlaSerG 12	HisGluargLeuargAlaGluProValGlyThrPheLeuValArgAsp 1(::: ::: ATGAAAACTTCGAGATACAGCAGACGGGACCTTTTGGTACGAGATGC 1:	euLeuAspAlaCysGlyPheTyrTrpGlyProLeuSerValHisGlyAla 90 ::: ::: ::: ::: ::: CTTACAAAATGCTGAATGGTACTGGGGAGATATCTCGAGGGAAGAAGTG 10	9ThrPheArgSerHisSerAspTyrArgArgIleThrArgThrSerAlaL 74	::: ::: ::: GAGCCTGCACCAGCACTGCCTCCTAAACCACCAAAACCTACT 987
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